Host ecology determines the dispersal patterns of a plant virus

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Supplementary Information

Supplementary Tables

Table 1: Log marginal likelihoods for molecular clock models

Molecular clock model	PS1	PS2	SS1	SS2
Exponential uncorrelated relaxed	-11685.20	-11694.13	-11694.25	-11697.49
Lognormal uncorrelated relaxed	-11667.00	-11670.96	-11669.92	-11669.32
Strict	-11683.93	-11679.56	-11692.06	-11681.71

PS: Path sampling

SS: Stepping-stone sampling

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Table 2: Log marginal likelihoods for discrete scenarios

Discrete diffusion model	PS1	PS2	SS1	SS2
Reversible	-306.87	-306.87	-306.44	-306.44
Reversible with BSSVS	-299.10	-299.17	-298.63	-298.71
Non-reversible	-309.08	-309.24	-308.65	-308.81
Non-reversible with BSSVS	-300.43	-300.226	-299.92	-299.70

PS: Path sampling

SS: Stepping-stone sampling

Table 3: Root location estimates for downsampled datasets for all discrete model scenarios

Subsampling method	Discrete diffusion model	Modal root location	Posterior probability
	Reversible	Tanzania	0.64
By diversity	Reversible with BSSVS	Tanzania	0.50
	Non-reversible	Tanzania	0.63
	Non-reversible with BSSVS	Tanzania	0.40
Randomly	Reversible	Tanzania	0.57
	Reversible with BSSVS	Tanzania	0.40
	Non-reversible	Tanzania	0.55
	Non-reversible with BSSVS	Tanzania	0.73

Table 4: GLM diffusion results for full data excluding resistance on harvested rice area as a potential predictor

Predictors	Bayes Factor	Log Conditional Effect Size	
Distance	> 9000	-1.082 [-1.4500.76]	
Origin of rice intensity in 1960	1.08	-1.74 [-3.260.49]	
Destination of rice intensity in 1960	0.011	0.02 [-0.64 - 0.95]	
Origin of rice intensity in 1990	7.21	$2.51 \ [0.64 - 5.60]$	
Destination of rice intensity in 1990	0.048	-0.45 [-1.01 - 0.015]	
Origin of precipitation	0.12	0.13 [-1.63 - 3.014]	
Destination of precipitation	0.01	-0.12 [-0.48 - 0.16]	
Origin of sample size	0.96	0.74 [0.23 - 2.47]	
Destination os sample size	1.15	0.62 [0.26 - 1.03]	

Values in between brackets represent 95% HPD intervals

Table 5: Log marginal likelihoods for distributions of continuous models

Model	PS1	PS2	SS1	SS2
Cauchy	-13283.67	-13267.39	-13251.18	-13236.09
Gamma	-13271.27	-13252.90	-13229.59	-13214.61
Lognormal	-13208.37	-13189.52	-13206.64	-13187.21
Homogeneous	-13494.189	-13457.77	-13448.06	-13427.39

PS: Path sampling

SS: Stepping-stone sampling

Supplementary Figures

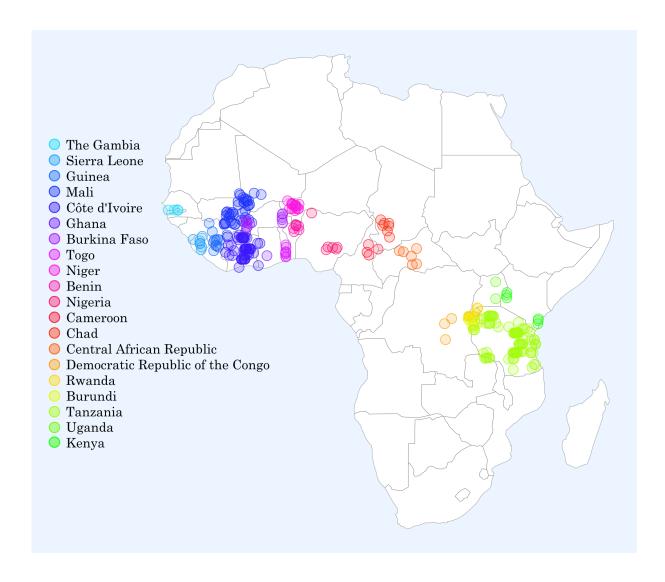


Figure 1: Continuous sampling of RYMV across Africa and respective legend representing the discrete locations assigned.



Figure 2: Maximum likelihood tree with selected clusters for visual temporal exploration.

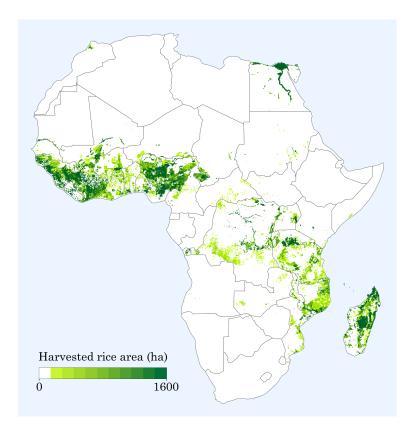


Figure 3: Harvested area (hectares) of rice in Africa in 2000, retrieved and adapted from HarvestChoice [1].

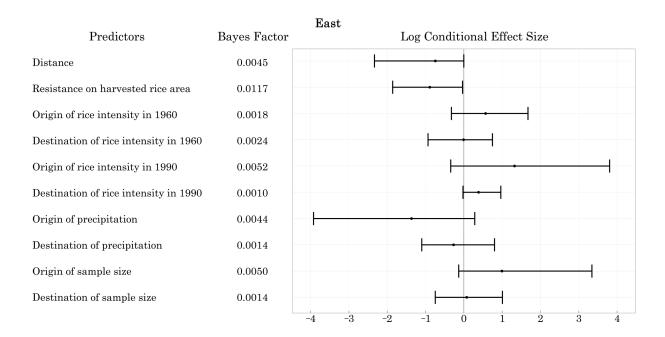


Figure 4: Predictors of RYMV dispersal sampled in East Africa. For each potential predictor, the Bayes factor (BF) support and the conditional effect sizes (cESs) obtained using the GLM diffusion approach implemented in BEAST are shown (posterior mean and 95% Bayesian credible interval, BCI).

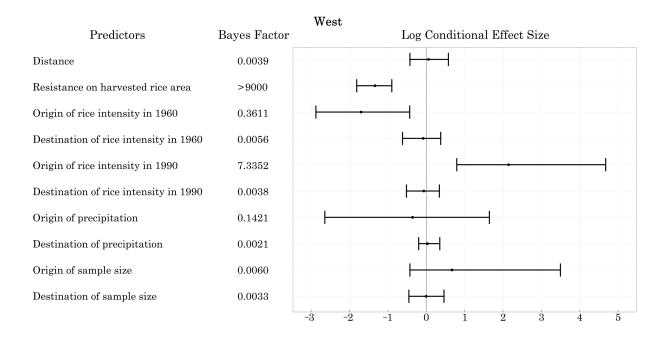


Figure 5: Predictors of RYMV dispersal sampled in West Africa. For each potential predictor, the Bayes factor (BF) support and the conditional effect sizes (cESs) obtained using the GLM diffusion approach implemented in BEAST are shown (posterior mean and 95% Bayesian credible interval, BCI). Note that the credible intervals for the cES of the predictors with BF>7 exclude zero, which can be considered as an additional indication for its importance.

References

[1] HarvestedChoice. Rice area harvested (ha) (2000). International Food Policy Research Institute, Washington, DC, and University of Minnesota, St Paul, MN Available online at http://harvestchoiceorg/node/4799. 2011;.